Patent claims:

1. A   degenerate   primer   constituent   from   the   group
    consisting of

        A-01f : gcsmrsgcstgg (Seq. ID NO. 1)
        B-01f : ggsctsccscc (Seq. ID NO. 2)
        B-01r : ggsggsagscc (Seq. ID NO. 3)
        C-01r : ggncgcwbsgg (Seq. ID NO. 4)
        A-01f : gcnmrrgcntgg (Seq. ID NO. 5)
        B-01f : ggnytnccncc (Seq. ID NO. 6)
        B-01r : ggnggnarncc (Seq. ID NO. 7)
        C-01r : gwngwrtccca (Seq. ID NO. 8)
        A-01f : gcntggrynga (Seq. ID NO. 9)
        B-01f : ggnytsccncc (Seq. ID NO. 10)
        B-01r : ggnggsarncc (Seq. ID NO. 11)
        C-01r : swnswrtccca (Seq. ID NO. 12).

2. A process for preparing protein sequences which are
    required for constructing the activity of a nitrile
    hydratase, such that
    a) a metagenome DNA library of a habitat is prepared,
    b) this library is contacted with in each case at
    least one forward(f) primer and one reverse(r) primer
    exhibiting a degenerate nucleic acid sequence as
    claimed in claim 1,
    c) a PCR is carried out using these primers,
    d) the full-length sequences of the nucleic acids
    encoding protein sequences which are required for
    constructing the activity of a nitrile hydratase are
    generated from the part sequences which are obtained,
    and
    e) these full-length sequences are cloned into a host
    organism and expressed.

3. The process as claimed in claim 2,
    characterized in that

in each case primer pairs composed of primers exhibiting the nucleic acid sequences A-01f and B-01r or C-01r and also B-01f and C-01r are used in the PCR.

5 4. The process as claimed in claim 2 and/or 3, characterized in that nucleic acid sequences selected from the group consisting of:

GCCAAGGTCGTC	(Seq. ID NO. 13)
GGCCGGTCCTG	(Seq. ID NO. 14)
TCCTTGTACCAGGTC	(Seq. ID NO. 15)
GCCCGCC	(Seq. ID NO. 16)
GGCGCTAATGTTGTT	(Seq. ID NO. 17)
TGGCCGGTTCTG	(Seq. ID NO. 18)
CAAATTCTTTATACCAAGTC	(Seq. ID NO. 19)
CCATATATCGCATTTCAGCT	(Seq. ID NO. 20)
GGTCGTGGCCAAG	(Seq. ID NO. 21)
GGCCGGTCCTG	(Seq. ID NO. 22)
TCCTTGTACCAGGTC	(Seq. ID NO. 23)
GCGCATTTCGGCG	(Seq. ID NO. 24)

are placed upstream of the degenerate nucleic acid sequences.

5. The process as claimed in one or more of the preceding claims 2 to 4, characterized in that use is made of primers which are selected from the group consisting of

GCCAAGGTCGTCgcsmrsgcstgg	(Seq. ID NO. 25)
GGCCGGTCCTGggsctsccscc	(Seq. ID NO. 26)
TCCTTGTACCAGGTCggsggsagscc	(Seq. ID NO. 27)
GCCCGCCggncgcwbsgg	(Seq. ID NO. 28)
GGCGCTAAAGTTGTTgcnmrrgcntgg	(Seq. ID NO. 29)
TGGCCGGTTCTGggnytnccncc	(Seq. ID NO. 30)
CAAATTCTTTATACCAAGTCggnggnarncc	(Seq. ID NO. 31)
CCATATATCGCATTTCAGCTgwngwrtcccca	(Seq. ID NO. 32)
GGTCGTGGCCAAGgcntggrynga	(Seq. ID NO. 33)

GGCCGGTCCTG<u>ggnytsccncc</u>   (Seq. ID NO. 34)

TCCTTGTACCAGGTC<u>ggnggsarncc</u>   (Seq. ID NO. 35)

GCGCATTTCGGCG<u>swnswrtccca</u>   (Seq. ID NO. 36).

6.   A protein sequence which is required for constructing
     the activity of a nitrile hydratase and which has less
     than 100% homology, at the amino acid level, with such
     known protein sequences, with the nucleic acid
     sequences encoding it being generated from part
     sequences which give a positive hybridization signal,
     under stringent conditions, with the primers
     exhibiting the nucleic acid sequences of claim 1.

7.   A nucleic acid sequence which encodes a protein
     sequence as claimed in claim 6.

8.   An expression system which exhibits one or more
     nucleic acid sequences as claimed in claim 7.

9.   A nitrile hydratase which exhibits protein sequences
     for α subunits and β subunits as claimed in claim 6.

10. The use of the nucleic acid sequences as claimed in
     claim 7 for producing improved protein sequences which
     are required for constructing the activity of a
     nitrile hydratase.

11. The use of the nitrile hydratases as claimed in
     claim 9 for preparing organic acid amides and acids.